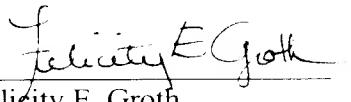


CONCLUSION

Applicants submit that the pending claims are in proper condition for allowance. Early notification to that effect is respectfully requested.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "**Version with markings to show changes made.**"

Respectfully submitted,

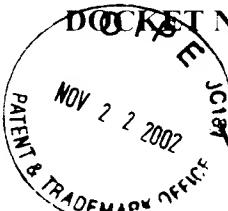


Felicity E. Groth
Registration No. 47,042

Date: November 2, 2002
WOODCOCK WASHBURN LLP
One Liberty Place - 46th Floor
Philadelphia, PA 19103
(215) 568-3100

Attachments

Paper Copy of the Substitute Sequence Listing
Substitute Sequence Listing in Computer Readable Form
Statement to Support Filing and Submission of Substitute Sequence Listing
Version with Markings to Show Changes Made



VERSION WITH MARKING TO SHOW CHANGES MADE

Please enter the following amendments:

IN THE SPECIFICATION:

The MMR proficient mouse H36 hybridoma cell line was transfected with various hPMS2 expression plasmids plus reporter constructs for assessing MMR activity. The MMR genes were cloned into the pEF expression vector, which contains the elongation factor promoter upstream of the cloning site followed by a mammalian polyadenylation signal. This vector also contains the NEO^r gene that allows for selection of cells retaining this plasmid. Briefly, cells were transfected with 1 μ g of each vector using polyliposomes following the manufacturer's protocol (Life Technologies). Cells were then selected in 0.5 mg/ml of G418 for 10 days and G418 resistant cells were pooled together to analyze for gene expression. The pEF construct contains an intron that separates the exon 1 of the EF gene from exon 2, which is juxtaposed to the 5' end of the polylinker cloning site. This allows for a rapid reverse transcriptase polymerase chain reaction (RT-PCR) screen for cells expressing the spliced products. At day 17, 100,000 cells were isolated and their RNA extracted using the trizol method as previously described (Nicolaides N.C., Kinzler, K.W., and Vogelstein, B. (1995) Analysis of the 5' region of PMS2 reveals heterogeneous transcripts and a novel overlapping gene. *Genomics* 29:329-334). RNAs were reverse transcribed using Superscript II (Life Technologies) and PCR amplified using a sense primer located in exon 1 of the EF gene (5'-ttt cgc aac ggg ttt gcc g-3') (SEQ ID NO: 17) and an antisense primer (5'-gtt tca gag tta agc ctt cg-3') (SEQ ID NO: 18) centered at nt 283 of the published human PMS2 cDNA, which will detect both the full length as well as the PMS134 gene expression. Reactions were carried out using buffers and conditions as previously described (Nicolaides, N.C., *et al.* (1995) Genomic organization of the human PMS2 gene family. *Genomics* 30:195-206), using the following amplification parameters: 94°C for 30 sec. 52°C for 2 min, 72°C for 2 min, for 30 cycles. Reactions were analyzed on agarose gels. Figure 1 shows a representative example of PMS expression in stably transduced H36 cells.

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IN THE SEQUENCE LISTING:

Please insert pages 1-26 of the Substitute Sequence Listing.

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371P _____
PCT Papers in a 371 Application

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Appendix

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